

**Amendments to the Specification:**

Please replace paragraph [0021] of the specification (US Patent Publication 20080229445) with the following amended paragraph:

[0021] A "cyclin A nucleic acid" as defined herein is taken to mean a nucleic acid encoding a protein which in its native form comprises motif 1, which is represented as: W L V/I E V S/A D/E D/E Y K/R/T L (SEQ ID NO: 6) (motif 1), where a backslash (/) means 'or', i.e. where 'V/I' means V or I. The presence of motif 1 in an amino acid sequence allows the sequence to be identified as a cyclin A rather than any other type of cyclin.

Please replace paragraph [0022] of the specification (US Patent Publication 20080229445) with the following amended paragraph:

[0022] The term "cyclin A2 nucleic acid" as defined herein is any nucleic acid encoding a protein which in its native form comprises motif 1 as identified above and additionally motif 2, which is represented as: E L T L V/I/T/M D/E/M Y T/S/H/P/G F R/L L/R/K/N F L P S (SEQ ID NO: 7) (motif 2), wherein the presence of at least two of the residues identified (T-----F--F---) (and underlined above) allow the sequence to be identified as a cyclin A2-type rather than as any other cyclin A. The dashes (-) above represent amino acid residues, where one dash is equal to one amino acid residue in a corresponding position in motif 2.

Please replace paragraph [0025] of the specification (US Patent Publication 20080229445) with the following amended paragraph:

[0025] The term "cyclin A2 amino acid" or "cyclin A2 protein" as defined herein is any amino acid which in its native form comprises motif 1 as identified above and additionally motif 2, which is represented as: E L T L V/I/T/M D/E/M Y T/S/H/P/G F R/L L/R/K/N F L P S (SEQ ID NO: 7) (motif 2), wherein the presence of at least two of the residues identified (T-----F--F---) (and underlined above) allow the sequence to be identified as a cyclin A2-type rather than as any other cyclin A. The dashes (-) above represent amino

acid residues, where one dash is equal to one amino acid residue in a corresponding position in motif 2.

Please replace paragraph [0048] of the specification (US Patent Publication 20080229445), with the following amended paragraph:

[0048] Orthologues in, for example, monocot plant species may easily be found by performing a so-called reciprocal blast search. This may be done by a first blast involving blasting the sequence in question (SEQ ID NO: 1 or SEQ ID NO: 2) against any sequence database, such as the publicly available NCBI database which may be found at: [http://www\[.\]ncbi.nlm.nih.gov](http://www[.]ncbi.nlm.nih.gov). If orthologues in rice were sought, the sequence in question would be blasted against, for example, the 28,469 full-length cDNA clones from *Oryza sativa* Nipponbare available at NCBI. BLASTn may be used when starting from nucleotides or TBLASTX when starting from the protein, with standard default values (expectation 10, alignment 50). The blast results may be filtered. The full-length sequences of either the filtered results or the non-filtered results are then blasted back (second blast) against the sequence in question (SEQ ID NO: 1 or 2). The results of the first and second blasts are then compared. In the case of large families, ClustalW is used followed by a neighbour joining tree to help visualize the clustering. Examples of cyclin A orthologues include the sequences deposited under the following accession numbers: a rice orthologue deposited under protein accession number AK106653 (cyclin A2 type), a rice orthologue deposited under protein accession number BAA86628 (cyclin A1 type) and a corn orthologue deposited under accession AAC50013.

Please replace paragraph [0086] of the specification (US Patent Publication 20080229445), with the following amended paragraph:

[0086] FIG. 3 is a table showing a cross-species conserved motif found in cyclin As. Motif 1 (SEQ ID NOs: 8-19) may be used to distinguish a cyclin A from any other type of cyclin and Motif 1 (SEQ ID NOs: 8-19) and Motif 2 (SEQ ID NOs: 20-31) together can be used to distinguish a A2 cyclin from any other A-type cyclin. By way of control, a motif found in cyclin B;1 is shown.

Please replace paragraph [0094] of the specification (US Patent Publication 20080229445), with the following amended paragraph:

[0094] The *Arabidopsis thaliana* cyclin A2;2 (internal reference CDS95) was amplified by PCR using as a template an *Arabidopsis thaliana* seedling cDNA library (Invitrogen, Paisley, UK). After reverse transcription of RNA extracted from seedlings, the cDNAs were cloned into pCMV Sport 6.0. Average insert size of the bank was 1.5 kb, and original number of clones was of 1.59.times.10.sup.7 cfu. Original titer was determined to be 9.6.times.10.sup.5 cfu/ml after first amplification of 6.times.10.sup.11 cfu/ml. After plasmid extraction, 200 ng of template was used in a 50 .mu.l PCR mix. Primers prm582 (sense, start codon in bold, AttB1 site in italic: 5' *ggggacaagttgtacaaaaagcaggcttcacaatgtattgctcttctcgatgc* 3') (SEQ ID NO:4) and prm583 (reverse, complementary, stop codon in bold, AttB2 site in italic: 5' *ggggaccactgtgtaacaagaagctgggtgcttggtgtcatcttgagaatag* 3') (SEQ ID NO:5), which include the AttB sites for Gateway recombination, were used for PCR amplification. PCR was performed using Hifi Taq DNA polymerase under standard conditions. A PCR fragment of 1311 bp was amplified and purified also using standard methods. The first step of the Gateway procedure, the BP reaction, was then performed, during which the PCR fragment recombined *in vivo* with the pDONR201 plasmid to produce, according to the Gateway terminology, an "entry clone", p754. Plasmid pDONR201 was purchased from Invitrogen, as part of the Gateway® technology.